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DIAGNOSTIC AND THERAPEUTIC USE OF A RAB FAMILY GTP-BINDING PROTEIN FOR NEURODEGENERATIVE DISEASES

The present invention relates to methods of diagnosing, prognosticating, and monitoring the progression of neurodegenerative diseases in a subject. Furthermore, methods of therapy control and screening for modulating agents of neurodegenerative diseases are provided. The invention also discloses pharmaceutical compositions, kits, and recombinant animal models.

Neurodegenerative diseases, in particular Alzheimer's disease (AD), have a strongly debilitating impact on a patient's life. Furthermore, these diseases constitute an enormous health, social, and economic burden. AD is the most common neurodegenerative disease, accounting for about 70% of all dementia cases, and it is probably the most devastating age-related neurodegenerative condition affecting about 10% of the population over 65 years of age and up to 45% over age 85 (for a recent review see Vickers et al., *Progress in Neurobiology* 2000, 60: 139-165). Presently, this amounts to an estimated 12 million cases in the US, Europe, and Japan. This situation will inevitably worsen with the demographic increase in the number of old people ("aging of the baby boomers") in developed countries. The neuropathological hallmarks that occur in the brains of individuals with AD are senile plaques, composed of amyloid-β protein, and profound cytoskeletal changes coinciding with the appearance of abnormal filamentous structures and the formation of neurofibrillary tangles.

The amyloid-β (Aβ) protein evolves from the cleavage of the amyloid precursor protein (APP) by different kinds of proteases. The cleavage by the β/γ-secretase leads to the formation of Aβ peptides of different lengths, typically a short more soluble and slow aggregating peptide consisting of 40 amino acids and a longer 42 amino acid peptide, which rapidly aggregates outside the cells, forming the characteristic amyloid plaques (Selkoe, *Physiological Rev* 2001, 81: 741-66; Greenfield et al., *Frontiers Bioscience* 2000, 5: D72-83). Two types of plaques, diffuse plaques and neuritic plaques, can be detected in the brain of AD patients, the latter ones being the classical, most prevalent type. They are primarily found in the cerebral cortex and hippocampus. The neuritic plaques have a diameter of 50μm to 200μm and are composed of insoluble fibrillar amyloids, fragments of dead

neurons, of microglia and astrocytes, and other components such as neurotransmitters, apolipoprotein E, glycosaminoglycans, α1-antichymotrypsin and others. The generation of toxic Aβ deposits in the brain starts very early in the course of AD, and it is discussed to be a key player for the subsequent destructive processes leading to AD pathology. The other pathological hallmarks of AD are neurofibrillary tangles (NFTs) and abnormal neurites, described as neuropil threads (Braak and Braak, *Acta Neuropathol* 1991, 82: 239-259). NFTs emerge inside neurons and consist of chemically altered tau, which forms paired helical filaments twisted around each other. Along the formation of NFTs, a loss of neurons can be observed. It is discussed that said neuron loss may be due to a damaged microtubule-associated transport system (Johnson and Jenkins, *J Alzheimers Dis* 1996, 1: 38-58; Johnson and Hartigan, *J Alzheimers Dis* 1999, 1: 329-351). The appearance of neurofibrillary tangles and their increasing number correlates well with the clinical severity of AD (Schmitt et al., *Neurology* 2000, 55: 370-376).

AD is a progressive disease that is associated with early deficits in memory formation and ultimately leads to the complete erosion of higher cognitive function. The cognitive disturbances include among other things memory impairment, aphasia, agnosia and the loss of executive functioning. A characteristic feature of the pathogenesis of AD is the selective vulnerability of particular brain regions and subpopulations of nerve cells to the degenerative process. Specifically, the temporal lobe region and the hippocampus are affected early and more severely during the progression of the disease. On the other hand, neurons within the frontal cortex, occipital cortex, and the cerebellum remain largely intact and are protected from neurodegeneration (Terry et al., *Annals of Neurology* 1981, 10: 184-92).

The age of onset of AD may vary within a range of 50 years, with early-onset AD occurring in people younger than 65 years of age, and late-onset of AD occurring in those older than 65 years. About 10% of all AD cases suffer from early-onset AD, with only 1-2% being familial, inherited cases.

Currently, there is no cure for AD, nor is there an effective treatment to halt the progression of AD or even to diagnose AD ante-mortem with high probability. Several risk factors have been identified that predispose an individual to develop AD, among them most prominently the epsilon 4 allele of the three different existing alleles (epsilon 2, 3, and 4) of the apolipoprotein E gene (ApoE) (Strittmatter et al., *Proc Natl Acad Sci USA* 1993, 90: 1977-81; Roses, *Ann NY Acad Sci* 1998, 855: 738-43). The polymorphic plasmaprotein ApoE plays a role in the intercellular cholesterol and phospholipid transport by binding low-density lipoprotein receptors,

and it seems to play a role in neurite growth and regeneration. Efforts to detect further susceptibility genes and disease-linked polymorphisms, lead to the assumption that specific regions and genes on human chromosomes 10 and 12 may be associated with late-onset AD (Myers et al., *Science* 2000, 290: 2304-5; Bertram et al., *Science* 2000, 290: 2303; Scott et al., *Am J Hum Genet* 2000, 66: 922-32). Although there are rare examples of early-onset AD which have been attributed to genetic defects in the genes for amyloid precursor protein (APP) on chromosome 21, presenilin-1 on chromosome 14, and presenilin-2 on chromosome 1, the prevalent form of late-onset sporadic AD is of hitherto unknown etiologic origin. The mutations found to date account for only half of the familial AD cases, which is less than 2% of all AD patients. The late onset and complex pathogenesis of neurodegenerative disorders pose a formidable challenge to the development of therapeutic and diagnostic agents. It is crucial to expand the pool of potential drug targets and diagnostic markers. It is therefore an object of the present invention to provide insight into the pathogenesis of neurological diseases and to provide methods, materials, agents, compositions, and animal models which are suited inter alia for the diagnosis and development of a treatment of these diseases. This object has been solved by the features of the independent claims. The subclaims define preferred embodiments of the present invention.

In the present invention, the detection and differential expression of a gene coding for the small GTP-binding protein rab31 is detected in human Alzheimer's disease brain samples by using an unbiased and sensitive suppressive subtractive hybridization approach and screening of DNA biochips. The exocytotic and endocytotic pathways of vesicles, granules and organelles is a highly regulated process in cells. The spatial and temporal distribution of these cargoes is regulated, for instance, by the activity of small monomeric GTP-ases, called rab proteins (for review: Zerial and McBride, *Nature Rev. Cell. Biol.* 2001, 2: 107-117). These rab proteins are involved in diverse processes such as vesicle formation, vesicle and organelle motility, and tethering of vesicles to their target compartments. Thereby the rab proteins switch from a GTP-bound active to a GDP-bound inactive form. This process is facilitated by the action of GTPase activating proteins (GAPs) in the target-membrane. Rab-proteins are located at the membrane of organelles via a 20-carbon geranyl-geranyl lipid anchor which is covalently attached to a cysteine-residue in the carboxy-terminus of the proteins by Rab-geranylgeranyltransferase. The prenylation is essential for correct membrane localization and function of the

rab-proteins. Integration into membranes is facilitated by so called Rab escort proteins (REPs) which are in involved in transfering newly synthesized rab-proteins to their target organelles where they interact with the SNARE factors which serve as multi protein complexes involved in vesicle targeting and vesicle fusion. Over 50 different rab-proteins have been detected so far (Pereira-Leal and Seabra, *J. Mol. Biol.* 2000, 301: 1077-1087), and they are thought to be localized to distinct intracellular membrane compartments fulfilling specific tasks and functions.

The ras-related protein rab31 was originally cloned from human melanocytes and designated rab22b (Chen et al., *Gene* 1996, 174: 129-134; NCBI GenBank entry: AF183421, mRNA 3969 bp). It shares the conserved GTP-binding domains I-IV, which are common to GTP-binding proteins like e.g. ras, and the cysteine-residues in the C-terminal domain. The open reading frame consists of 585 base pairs coding for a polypeptide of 194 amino acids in length and with a molecular weight of 21.6 kDa (GenBank accession number Q13636). It thus represents one of the smallest rab-proteins known so far. Two transcription products coding for rab31 were detected in human tissue (Chen et al., *Gene* 1996, 174: 129-134). The major transcript of about 4.0 kb is expressed ubiquitously and abundantly in a wide variety of human tissues. An additional minor 1.0 kb-transcript is detected in tissues with relatively high expression levels, such as testis, ovary, lung, and leukocytes. The gene was subsequently mapped to human chromosome 18. An almost identical cDNA was cloned from human platelets and designated rab31 (Bao et al., *Eur. J. Biochem.* 2002, 269: 259-271; NCBI GenBank protein entry: AAB02832; NCBI GenBank entry for nucleotide sequence of rab31 cDNA: U59877, Q13636). This protein differs by two nucleotides in the C-terminal region compared to the above mentioned rab22b giving rise to an amino acid exchange (rab31 as disclosed in this application is identical to the protein as published in Bao et al. 2002). The expression of rab31 is most strongly in human brain and placenta and could be detected also in heart and lung whereas no expression was visible in liver, skeletal muscle, kidney and pancreas. Subcellular distribution analysis revealed that rab31 is associated with intracellular membranes rather than being present in the cytosolic fraction (Bao et al., Eur. J. Biochem. 2002, 269: 259-271).

Based on the above information it is reasonable to assume that rab31, as a vesicle membrane-associated protein, participates in the regulation of vesicle trafficking, targeting and fusion. Rab31 may, for instance, impact on sorting and targeting of transport vesicles containing the amyloid precursor protein (APP) and, thereby, have a causative role in the development of AD.

The present invention discloses a dysregulation of rab31 gene expression on the transcriptional level in the temporal cortex region relative to the frontal cortex region of brain samples taken from AD patients. No such dysregulation is observed in samples derived from age-matched, healthy controls. To date, no experiments have been described that demonstrate a relationship between a dysregulation of rab31 gene expression and the pathology of neuro-degenerative diseases, in particular AD. Such a link, as disclosed in the present invention, offers new ways, inter alia, for the diagnosis and treatment of said diseases.

The singular forms "a", "an", and "the" as used herein and in the claims include plural reference unless the context dictates otherwise. For example, "a cell" means as well a plurality of cells, and so forth. The term "and/or" as used in the present specification and in the claims implies that the phrases before and after this term are to be considered either as alternatives or in combination. For instance, the wording "determination of a level and/or an activity" means that either only a level, or only an activity, or both a level and an activity are determined. The term "level" as used herein is meant to comprise a gage of, or a measure of the amount of, or a concentration of a transcription product, for instance an mRNA, or a translation product, for instance a protein or polypeptide. The term "activity" as used herein shall be understood as a measure for the ability of a transcription product or a translation product to produce a biological effect or a measure for a level of biologically active molecules. The term "activity" also refers to enzymatic activity. The terms "level" and/or "activity" as used herein further refer to gene expression levels or gene activity. Gene expression can be defined as the utilization of the information contained in a gene by transcription and translation leading to the production of a gene product. "Dysregulation" shall mean an upregulation or downregulation of gene expression. A gene product comprises either RNA or protein and is the result of expression of a gene. The amount of a gene product can be used to measure how active a gene is. The term "gene" as used in the present specification and in the claims comprises both coding regions (exons) as well as non-coding regions (e.g. non-coding regulatory elements such as promoters or enhancers, introns, leader and trailer sequences). The term "ORF" is an acronym for "open reading frame" and refers to a nucleic acid sequence that does not possess a stop codon in at least one reading frame and therefore can potentially be translated into a sequence of amino acids. "Regulatory elements" shall comprise inducible and

non-inducible promoters, enhancers, operators, and other elements that drive and regulate gene expression. The term "fragment" as used herein is meant to comprise e.g. an alternatively spliced, or truncated, or otherwise cleaved transcription product or translation product. The term "derivative" as used herein refers to a mutant, or an RNA-edited, or a chemically modified, or otherwise altered transcription product, or to a mutant, or chemically modified, or otherwise altered translation product. For instance, a "derivative" may be generated by processes such as altered phosphorylation, or glycosylation, or acetylation, or lipidation, or by altered signal peptide cleavage or other types of maturation cleavage. These processes may occur post-translationally. The term "modulator" as used in the present invention and in the claims refers to a molecule capable of changing or altering the level and/or the activity of a gene, or a transcription product of a gene, or a translation product of a gene. Preferably, a "modulator" is capable of changing or altering the biological activity of a transcription product or a translation product of a gene. Said modulation, for instance, may be an increase or a decrease in enzyme activity, a change in binding characteristics, or any other change or alteration in the biological, functional, or immunological properties of said translation product of a gene. The terms "agent", "reagent", or "compound" refer to any substance, chemical, composition or extract that have a positive or negative biological effect on a cell, tissue, body fluid, or within the context of any biological system, or any assay system examined. They can be agonists, antagonists, partial agonists or inverse agonists of a target. Such agents, reagents, or compounds may be nucleic acids, natural or synthetic peptides or protein complexes, or fusion proteins. They may also be antibodies, organic or anorganic molecules or compositions, small molecules, drugs and any combinations of any of said agents above. They may be used for testing, for diagnostic or for therapeutic purposes. The terms "oligonucleotide primer" or "primer" refer to short nucleic acid sequences which can anneal to a given target polynucleotide by hybridization of the complementary base pairs and can be extended by a polymerase. They may be chosen to be specific to a particular sequence or they may be randomly selected, e.g. they will prime all possible sequences in a mix. The length of primers used herein may vary from 10 nucleotides to 80 nucleotides. "Probes" are short nucleic acid sequences of the nucleic acid sequences described and disclosed herein or sequences complementary therewith. They may comprise full length sequences, or fragments, derivatives, isoforms, or variants of a given sequence. The identification of hybridization complexes between a "probe" and an assayed sample allows the detection of the presence of other

similar sequences within that sample. As used herein, "homolog or homology" is a term used in the art to describe the relatedness of a nucleotide or peptide sequence to another nucleotide or peptide sequence, which is determined by the degree of identity and/or similarity between said sequences compared. The term "variant" as used herein refers to any polypeptide or protein, in reference to polypeptides and proteins disclosed in the present invention, in which one or more amino acids are added and/or substituted and/or deleted and/or inserted at the N-terminus, and/or the C-terminus, and/or within the native amino acid sequences of the native polypeptides or proteins of the present invention. Furthermore, the term "variant" shall include any shorter or longer version of a polypeptide or protein. "Variants" shall also comprise a sequence that has at least about 80% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% sequence identity with the amino acid sequences of SEQ ID NO.1. "Variants" of a protein molecule shown in SEQ ID NO. 1 include, for example, proteins with conservative amino acid substitutions in highly conservative regions. "Proteins and polypeptides" of the present invention include variants, fragments and chemical derivatives of the protein comprising SEQ ID NO. 1. They can include proteins and polypeptides which can be isolated from nature or be produced by recombinant and/or synthetic means. Native proteins or polypeptides refer to naturally-occurring truncated or secreted forms, naturally occurring variant forms (e.g. splice-variants) and naturally occurring allelic variants. The term "isolated" as used herein is considered to refer to molecules that are removed from their natural environment, i.e. isolated from a cell or from a living organism in which they normally occur, and that are separated or essentially purified from the coexisting components with which they are found to be associated in nature. This notion further means that the sequences encoding such molecules can be linked by the hand of man to polynucleotides, to which they are not linked in their natural state, and that such molecules can be produced by recombinant and/or synthetic means. Even if for said purposes those sequences may be introduced into living or non-living organisms by methods known to those skilled in the art, and even if those sequences are still present in said organisms, they are still considered to be isolated. In the present invention, the terms "risk", "susceptibility", and "predisposition" are tantamount and are used with respect to the probability of developing a neurodegenerative disease, preferably Alzheimer's disease.

The term 'AD' shall mean Alzheimer's disease. "AD-type neuropathology" as used herein refers to neuropathological, neurophysiological, histopathological and clinical

hallmarks as described in the instant invention and as commonly known from state-of-the-art literature (see: Iqbal, Swaab, Winblad and Wisniewski, *Alzheimer's Disease and Related Disorders (Etiology, Pathogenesis and Therapeutics)*, Wiley & Sons, New York, Weinheim, Toronto, 1999; Scinto and Daffner, *Early Diagnosis of Alzheimer's Disease*, Humana Press, Totowa, New Jersey, 2000; Mayeux and Christen, *Epidemiology of Alzheimer's Disease: From Gene to Prevention*, Springer Press, Berlin, Heidelberg, New York, 1999; Younkin, Tanzi and Christen, *Presenilins and Alzheimer's Disease*, Springer Press, Berlin, Heidelberg, New York, 1998). Neurodegenerative diseases or disorders according to the present invention comprise Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, Pick's disease, fronto-temporal dementia, progressive nuclear palsy, corticobasal degeneration, cerebro-vascular dementia, multiple system atrophy, argyrophilic grain dementia and other tauopathies, and mild-cognitive impairment. Further conditions involving neurodegenerative processes are, for instance, age-related macular degeneration, narcolepsy, motor neuron diseases, prion diseases, traumatic nerve injury and repair, and multiple sclerosis.

In one aspect, the invention features a method of diagnosing or prognosticating a neurodegenerative disease in a subject, or determining whether a subject is at increased risk of developing said disease. The method comprises: determining a level, or an activity, or both said level and said activity of (i) a transcription product of a gene coding for rab31, and/or of (ii) a translation product of a gene coding for rab31, and/or of (iii) a fragment, or derivative, or variant of said transcription or translation product in a sample from said subject and comparing said level, and/or said activity to a reference value representing a known disease or health status, thereby diagnosing or prognosticating said neurodegenerative disease in said subject, or determining whether said subject is at increased risk of developing said neurodegenerative disease.

The invention also relates to the construction and the use of primers and probes which are unique to the nucleic acid sequences, or fragments, or variants thereof, as disclosed in the present invention. The oligonucleotide primers and/or probes can be labeled specifically with fluorescent, bioluminescent, magnetic, or radioactive substances. The invention further relates to the detection and the production of said nucleic acid sequences, or fragments and variants thereof, using said specific

oligonucleotide primers in appropriate combinations. PCR-analysis, a method well known to those skilled in the art, can be performed with said primer combinations to amplify said gene specific nucleic acid sequences from a sample containing nucleic acids. Such sample may be derived either from healthy or diseased subjects. Whether an amplification results in a specific nucleic acid product or not, and whether a fragment of different length can be obtained or not, may be indicative for a neurodegenerative disease, in particular Alzheimer's disease. Thus, the invention provides nucleic acid sequences, oligonucleotide primers, and probes of at least 10 bases in length up to the entire coding and gene sequences, useful for the detection of gene mutations and single nucleotide polymorphisms in a given sample comprising nucleic acid sequences to be examined, which may be associated with neurodegenerative diseases, in particular Alzheimer's disease. This feature has utility for developing rapid DNA-based diagnostic tests, preferably also in the format of a kit.

In a further aspect, the invention features a method of monitoring the progression of a neurodegenerative disease in a subject. A level, or an activity, or both said level and said activity, of (i) a transcription product of a gene coding for rab31, and/or of (ii) a translation product of a gene coding for rab31, and/or of (iii) a fragment, or derivative, or variant of said transcription or translation product in a sample from said subject is determined. Said level and/or said activity is compared to a reference value representing a known disease or health status. Thereby the progression of said neurodegenerative disease in said subject is monitored.

In still a further aspect, the invention features a method of evaluating a treatment for a neurodegenerative disease, comprising determining a level, or an activity, or both said level and said activity of (i) a transcription product of a gene coding for rab31, and/or of (ii) a translation product of a gene coding for rab31, and/or of (iii) a fragment, or derivative, or variant of said transcription or translation product in a sample obtained from a subject being treated for said disease. Said level, or said activity, or both said level and said activity are compared to a reference value representing a known disease or health status, thereby evaluating the treatment for said neurodegenerative disease.

In a preferred embodiment of the herein claimed methods, kits, recombinant animals, molecules, assays, and uses of the instant invention, said gene coding for

a small GTP-binding protein, is a gene coding for the ras-related protein rab31, also termed rab22b, represented by SEQ ID NO. 1, or fragments, derivatives, or variants thereof (GenBank accession number Q13636; mRNA GenBank accession number AF183421).

In a further preferred embodiment of the herein claimed methods, kits, recombinant animals, molecules, assays, and uses of the instant invention, said neurodegenerative disease or disorder is Alzheimer's disease, and said subjects suffer from Alzheimer's disease.

The present invention discloses the detection and differential expression and regulation of a gene coding for rab31 in specific brain regions of AD patients. Consequently, the rab31 gene and its corresponding transcription and/or translation products may have a causative role in the regional selective neuronal degeneration typically observed in AD. Alternatively, rab31 may confer a neuroprotective function to the remaining surviving nerve cells. Based on these disclosures, the present invention has utility for the diagnostic evaluation and prognosis as well as for the identification of a predisposition to a neurodegenerative disease, in particular AD. Furthermore, the present invention provides methods for the diagnostic monitoring of patients undergoing treatment for such a disease.

It is particularly preferred that said sample to be analyzed and determined is selected from the group comprising brain tissue, or other tissues, or body cells. The sample can also comprise cerebrospinal fluid or other body fluids including saliva, urine, blood, serum plasma, or mucus. Preferably, the methods of diagnosis, prognosis, monitoring the progression or evaluating a treatment for a neurodegenerative disease, according to the instant invention, can be practiced *ex corpore*, and such methods preferably relate to samples, for instance, body fluids or cells, removed, collected, or isolated from a subject or patient.

In further preferred embodiments, said reference value is that of a level, or an activity, or both said level and said activity of (i) a transcription product of a gene coding for rab31, and/or of (ii) a translation product of a gene coding for rab31, and/or of (iii) a fragment, or derivative, or variant of said transcription or translation product in a sample from a subject not suffering from said neurodegenerative disease.

In preferred embodiments, an alteration in the level and/or activity of a transcription product of a gene coding for rab31, and/or of a translation product of a gene coding for rab31, and/or of a fragment, or derivative, or variant thereof in a sample cell, or tissue, or body fluid from said subject relative to a reference value representing a known health status indicates a diagnosis, or prognosis, or increased risk of becoming diseased with a neurodegenerative disease, particularly AD.

In preferred embodiments, measurement of the level of transcription products of a rab31 gene is performed in a sample from a subject using a quantitative PCR-analysis with primer combinations to amplify said gene specific sequences from cDNA obtained by reverse transcription of RNA extracted from a sample of a subject. A Northern blot with probes specific for said gene can also be applied. It might further be preferred to measure transcription products by means of chip-based microarray technologies. These techniques are known to those of ordinary skill in the art (see Sambrook and Russell, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 2001; Schena M., *Microarray Biochip Technology*, Eaton Publishing, Natick, MA, 2000). An example of an immunoassay is the detection and measurement of enzyme activity as disclosed and described in the patent application WO 02/14543.

Furthermore, a level and/or an activity of a translation product of a rab31 gene and/or of a fragment, or derivative, or variant of said translation product, and/or a level of activity of said translation product, and/or of a fragment, or derivative, or variant thereof, can be detected using an immunoassay, an activity assay, and/or a binding assay. These assays can measure the amount of binding between said protein molecule and an anti-protein antibody by the use of enzymatic, chromodynamic, radioactive, magnetic, or luminescent labels which are attached to either the anti-protein antibody or a secondary antibody which binds the anti-protein antibody. In addition, other high affinity ligands may be used. Immunoassays which can be used include e.g. ELISAs, Western blots, and other techniques known to those of ordinary skill in the art (see Harlow and Lane, *Using Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1999 and Edwards R, *Immunodiagnostics: A Practical Approach*, Oxford University Press, Oxford; England, 1999). All these detection techniques may also be employed in the format of microarrays, protein-arrays, antibody microarrays,

tissue microarrays, electronic biochip or protein-chip based technologies (see Schena M., *Microarray Biochip Technology*, Eaton Publishing, Natick, MA, 2000).

In a preferred embodiment, the level, or the activity, or both said level and said activity of (i) a transcription product of a gene coding for rab31, and/or of (ii) a translation product of a gene coding for rab31, and/or of (iii) a fragment, or derivative, or variant of said transcription or translation product in a series of samples taken from said subject over a period of time is compared, in order to monitor the progression of said disease. In further preferred embodiments, said subject receives a treatment prior to one or more of said sample gatherings. In yet another preferred embodiment, said level and/or activity is determined before and after said treatment of said subject.

In another aspect, the invention features a kit for diagnosing or prognosticating neurodegenerative diseases, in particular AD, in a subject, or determining the propensity or predisposition of a subject to develop a neurodegenerative disease, in particular AD, said kit comprising:
(a) at least one reagent which is selected from the group consisting of (i) reagents that selectively detect a transcription product of a gene coding for rab31, and (ii) reagents that selectively detect a translation product of a gene coding for rab31; and
(b) an instruction for diagnosing or prognosticating a neurodegenerative disease, in particular AD, or determining the propensity or predisposition of a subject to develop such a disease by
- detecting a level, or an activity, or both said level and said activity, of said transcription product and/or said translation product of a gene coding for rab31, in a sample from said subject; and
- diagnosing or prognosticating a neurodegenerative disease, in particular AD, or determining the propensity or predisposition of said subject to develop such a disease,
wherein a varied level, or activity, or both said level and said activity, of said transcription product and/or said translation product compared to a reference value representing a known health status; or a level, or activity, or both said level and said activity, of said transcription product and/or said translation product similar or equal to a reference value representing a known disease status, indicates a diagnosis or prognosis of a neurodegenerative disease, in particular AD, or an increased propensity or predisposition of developing such a disease. The kit, according to the

present invention, may be particularly useful for the identification of individuals that are at risk of developing a neurodegenerative disease, in particular AD. Consequently, the kit, according to the invention, may serve as a means for targeting identified individuals for early preventive measures or therapeutic intervention prior to disease onset, before irreversible damage in the course of the disease has been inflicted. Furthermore, in preferred embodiments, the kit featured in the invention is useful for monitoring a progression of a neurodegenerative disease, in particular AD, in a subject, as well as monitoring success or failure of therapeutic treatment for such a disease of said subject.

In another aspect, the invention features a method of treating or preventing a neurodegenerative disease, in particular AD, in a subject comprising the administration to said subject in a therapeutically or prophylactically effective amount of an agent or agents which directly or indirectly affect a level, or an activity, or both said level and said activity, of (i) a gene coding for rab31, and/or (ii) a transcription product of a gene coding for rab31, and/or (iii) a translation product of a gene coding for rab31, and/or (iv) a fragment, or derivative, or variant of (i) to (iii). Said agent may comprise a small molecule, or it may also comprise a peptide, an oligopeptide, or a polypeptide. Said peptide, oligopeptide, or polypeptide may comprise an amino acid sequence of SEQ ID NO. 1, or a fragment, or derivative, or a variant thereof. An agent for treating or preventing a neurodegenerative disease, in particular AD, according to the instant invention, may also consist of a nucleotide, an oligonucleotide, or a polynucleotide. Said oligonucleotide or polynucleotide may comprise a nucleotide sequence of the gene coding for a rab31 protein, either in sense orientation or in antisense orientation.

In preferred embodiments, the method comprises the application of per se known methods of gene therapy and/or antisense nucleic acid technology to administer said agent or agents. In general, gene therapy includes several approaches: molecular replacement of a mutated gene, addition of a new gene resulting in the synthesis of a therapeutic protein, and modulation of endogenous cellular gene expression by recombinant expression methods or by drugs. Gene-transfer techniques are described in detail (see e.g. Behr, *Acc Chem Res* 1993, 26: 274-278 and Mulligan, *Science* 1993, 260: 926-931) and include direct gene-transfer techniques such as mechanical microinjection of DNA into a cell as well as indirect techniques employing biological vectors (like recombinant viruses, especially

retroviruses) or model liposomes, or techniques based on transfection with DNA coprecipitation with polycations, cell membrane pertubation by chemical (solvents, detergents, polymers, enzymes) or physical means (mechanic, osmotic, thermic, electric shocks). The postnatal gene transfer into the central nervous system has been described in detail (see e.g. Wolff, *Curr Opin Neurobiol* 1993, 3: 743-748).

In particular, the invention features a method of treating or preventing a neurodegenerative disease by means of antisense nucleic acid therapy, i.e. the down-regulation of an inappropriately expressed or defective gene by the introduction of antisense nucleic acids or derivatives thereof into certain critical cells (see e.g. Gillespie, *DN&P* 1992, 5: 389-395; Agrawal and Akhtar, *Trends Biotechnol* 1995, 13: 197-199; Crooke, *Biotechnology* 1992, 10: 882-6). Apart from hybridization strategies, the application of ribozymes, i.e. RNA molecules that act as enzymes, destroying RNA that carries the message of disease has also been described (see e.g. Barinaga, *Science* 1993, 262: 1512-1514). In preferred embodiments, the subject to be treated is a human, and therapeutic antisense nucleic acids or derivatives thereof are directed against transcripts of a gene coding for rab31. It is preferred that cells of the central nervous system, preferably the brain, of a subject are treated in such a way. Cell penetration can be performed by known strategies such as coupling of antisense nucleic acids and derivatives thereof to carrier particles, or the above described techniques. Strategies for administering targeted therapeutic oligodeoxynucleotides are known to those of skill in the art (see e.g. Wickstrom, *Trends Biotechnol* 1992, 10: 281-287). In some cases, delivery can be performed by mere topical application. Further approaches are directed to intracellular expression of antisense RNA. In this strategy, cells are transformed *ex vivo* with a recombinant gene that directs the synthesis of an RNA that is complementary to a region of target nucleic acid. Therapeutical use of intracellularly expressed antisense RNA is procedurally similar to gene therapy. A recently developed method of regulating the intracellular expression of genes by the use of double-stranded RNA, known variously as RNA interference (RNAi), can be another effective approach for nucleic acid therapy (Hannon, *Nature* 2002, 418: 244-251).

In further preferred embodiments, the method comprises grafting donor cells into the central nervous system, preferably the brain, of said subject, or donor cells preferably treated so as to minimize or reduce graft rejection, wherein said donor cells are genetically modified by insertion of at least one transgene encoding said

agent or agents. Said transgene might be carried by a viral vector, in particular a retroviral vector. The transgene can be inserted into the donor cells by a nonviral physical transfection of DNA encoding a transgene, in particular by microinjection. Insertion of the transgene can also be performed by electroporation, chemically mediated transfection, in particular calcium phosphate transfection, or liposomal mediated transfection (see Mc Celland and Pardee, *Expression Genetics: Accelerated and High-Throughput Methods*, Eaton Publishing, Natick, MA, 1999).

In preferred embodiments, said agent for treating and preventing a neurodegenerative disease, in particular AD, is a therapeutic protein which can be administered to said subject, preferably a human, by a process comprising introducing subject cells into said subject, said subject cells having been treated *in vitro* to insert a DNA segment encoding said therapeutic protein, said subject cells expressing *in vivo* in said subject a therapeutically effective amount of said therapeutic protein. Said DNA segment can be inserted into said cells *in vitro* by a viral vector, in particular a retroviral vector.

Methods of treatment, according to the present invention, comprise the application of therapeutic cloning, transplantation, and stem cell therapy using embryonic stem cells or embryonic germ cells and neuronal adult stem cells, combined with any of the previously described cell- and gene therapeutic methods. Stem cells may be totipotent or pluripotent. They may also be organ-specific. Strategies for repairing diseased and/or damaged brain cells or tissue comprise (i) taking donor cells from an adult tissue. Nuclei of those cells are transplanted into unfertilized egg cells from which the genetic material has been removed. Embryonic stem cells are isolated from the blastocyst stage of the cells which underwent somatic cell nuclear transfer. Use of differentiation factors then leads to a directed development of the stem cells to specialized cell types, preferably neuronal cells (Lanza et al., *Nature Medicine* 1999, 9: 975-977), or (ii) purifying adult stem cells, isolated from the central nervous system, or from bone marrow (mesenchymal stem cells), for in vitro expansion and subsequent grafting and transplantation, or (iii) directly inducing endogenous neural stem cells to proliferate, migrate, and differentiate into functional neurons (Peterson DA, *Curr. Opin. Pharmacol.* 2002, 2: 34-42). Adult neural stem cells are of great potential for repairing damaged or diseased brain tissues, as the germinal centers of the adult brain are free of neuronal damage or dysfunction (Colman A, *Drug Discovery World* 2001, 7: 66-71).

In preferred embodiments, the subject for treatment or prevention, according to the present invention, can be a human, an experimental animal, e.g. a mouse or a rat, a domestic animal, or a non-human primate. The experimental animal can be an animal model for a neurodegenerative disorder, e.g. a transgenic mouse and/or a knock-out mouse with an AD-type neuropathology.

In a further aspect, the invention features a modulator of an activity, or a level, or both said activity and said level of at least one substance which is selected from the group consisting of (i) a gene coding for rab31, and/or (ii) a transcription product of a gene coding for rab31 and/or (iii) a translation product of a gene coding for rab31, and/or (iv) a fragment, or derivative, or variant of (i) to (iii).

In an additional aspect, the invention features a pharmaceutical composition comprising said modulator and preferably a pharmaceutical carrier. Said carrier refers to a diluent, adjuvant, excipient, or vehicle with which the modulator is administered.

In a further aspect, the invention features a modulator of an activity, or a level, or both said activity and said level of at least one substance which is selected from the group consisting of (i) a gene coding for rab31, and/or (ii) a transcription product of a gene coding for rab31, and/or (iii) a translation product of a gene coding for rab31, and/or (iv) a fragment, or derivative, or variant of (i) to (iii) for use in a pharmaceutical composition.

In another aspect, the invention provides for the use of a modulator of an activity, or a level, or both said activity and said level of at least one substance which is selected from the group consisting of (i) a gene coding for rab31, and/or (ii) a transcription product of a gene coding for rab31 and/or (iii) a translation product of a gene coding for rab31, and/or (iv) a fragment, or derivative, or variant of (i) to (iii) for a preparation of a medicament for treating or preventing a neurodegenerative disease, in particular AD.

In one aspect, the present invention also provides a kit comprising one or more containers filled with a therapeutically or prophylactically effective amount of said pharmaceutical composition.

In a further aspect, the invention features a recombinant, non-human animal comprising a non-native gene sequence coding for rab31, or a fragment, or derivative, or variant thereof. The generation of said recombinant, non-human animal comprises (i) providing a gene targeting construct containing said gene sequence and a selectable marker sequence, and (ii) introducing said targeting construct into a stem cell of a non-human animal, and (iii) introducing said non-human animal stem cell into a non-human embryo, and (iv) transplanting said embryo into a pseudopregnant non-human animal, and (v) allowing said embryo to develop to term, and (vi) identifying a genetically altered non-human animal whose genome comprises a modification of said gene sequence in both alleles, and (vii) breeding the genetically altered non-human animal of step (vi) to obtain a genetically altered non-human animal whose genome comprises a modification of said endogenous gene, wherein said gene is mis-expressed, or under-expressed, or over-expressed, and wherein said disruption or alteration results in said non-human animal exhibiting a predisposition to developing symptoms of neuropathology similar to a neurodegenerative disease, in particular AD. Strategies and techniques for the generation and construction of such an animal are known to those of ordinary skill in the art (see e.g. Capecchi, *Science* 1989, 244: 1288-1292 and Hogan et al., *Manipulating the Mouse Embryo: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1994 and Jackson and Abbott, *Mouse Genetics and Transgenics: A Practical Approach*, Oxford University Press, Oxford, England, 1999). It is preferred to make use of such a recombinant non-human animal as an animal model for investigating neurodegenerative diseases, in particular Alzheimer's disease. Such an animal may be useful for screening, testing and validating compounds, agents and modulators in the development of diagnostics and therapeutics to treat neurodegenerative diseases, in particular Alzheimer's disease.

In another aspect, the invention features an assay for screening for a modulator of neurodegenerative diseases, in particular AD, or related diseases and disorders of one or more substances selected from the group consisting of (i) a gene coding for rab31, and/or (ii) a transcription product of a gene coding for rab31, and/or (iii) a translation product of a gene coding for rab31, and/or (iv) a fragment, or derivative, or variant of (i) to (iii). This screening method comprises (a) contacting a cell with a test compound, and (b) measuring the activity, or the level, or both the activity and

the level of one or more substances recited in (i) to (iv), and (c) measuring the activity, or the level, or both the activity and the level of said substances in a control cell not contacted with said test compound, and (d) comparing the levels of the substance in the cells of step (b) and (c), wherein an alteration in the activity and/or level of said substances in the contacted cells indicates that the test compound is a modulator of said diseases and disorders.

In one further aspect, the invention features a screening assay for a modulator of neurodegenerative diseases, in particular AD, or related diseases and disorders of one or more substances selected from the group consisting of (i) a gene coding for rab31, and/or (ii) a transcription product of a gene coding for rab31, and/or (iii) a translation product of a gene coding for rab31, and/or (iv) a fragment, or derivative, or variant of (i) to (iii), comprising (a) administering a test compound to a test animal which is predisposed to developing or has already developed symptoms of a neurodegenerative disease or related diseases or disorders, and (b) measuring the activity and/or level of one or more substances recited in (i) to (iv), and (c) measuring the activity and/or level of said substances in a matched control animal which is equally predisposed to developing or has already developed said symptoms and to which animal no such test compound has been administered, and (d) comparing the activity and/or level of the substance in the animals of step (b) and (c), wherein an alteration in the activity and/or level of substances in the test animal indicates that the test compound is a modulator of said diseases and disorders.

In a preferred embodiment, said test animal and/or said control animal is a recombinant, non-human animal which expresses a gene coding for rab31, or a fragment, or a derivative, or a variant thereof, under the control of a transcriptional regulatory element which is not the native rab31 gene transcriptional control regulatory element.

In another embodiment, the present invention provides a method for producing a medicament comprising the steps of (i) identifying a modulator of neurodegenerative diseases by a method of the aforementioned screening assays and (ii) admixing the modulator with a pharmaceutical carrier. However, said modulator may also be identifiable by other types of screening assays.

In another aspect, the present invention provides for an assay for testing a compound, preferably for screening a plurality of compounds, for inhibition of binding between a ligand and a translation product of a gene coding for rab31, or a fragment, or derivative, or variant thereof. Said screening assay comprises the steps of (i) adding a liquid suspension of said rab31 translation product, or a fragment, or derivative, or variant thereof, to a plurality of containers, and (ii) adding a compound or a plurality of compounds to be screened for said inhibition to said plurality of containers, and (iii) adding a detectable, preferably a fluorescently labelled ligand to said containers, and (iv) incubating said rab31 translation product, or said fragment, or derivative, or variant thereof, and said compound or plurality of compounds, and said detectable, preferably fluorescently labelled ligand, and (v) measuring the amounts of preferably fluorescence associated with said rab31 translation product, or with said fragment, or derivative, or variant thereof, and (vi) determining the degree of inhibition by one or more of said compounds of binding of said ligand to said rab31 translation product, or said fragment, or derivative, or variant thereof. It might be preferred to reconstitute said rab31 translation product, or fragment, or derivative, or variant thereof into artificial liposomes to generate the corresponding proteoliposomes to determine the inhibition of binding between a ligand and said rab31 translation product. Methods of reconstitution of rab31 translation products from detergent into liposomes have been detailed (Schwarz et al., *Biochemistry* 1999, 38: 9456-9464; Krivosheev and Usanov, *Biochemistry-Moscow* 1997, 62: 1064-1073). Instead of utilizing a fluorescently labelled ligand, it might in some aspects be preferred to use any other detectable label known to the person skilled in the art, e.g. radioactive labels, and detect it accordingly. Said method may be useful for the identification of novel compounds as well as for evaluating compounds which have been improved or otherwise optimized in their ability to inhibit the binding of a ligand to an rab31 translation product, or a fragment, or derivative, or variant thereof. One example of a fluorescent binding assay, in this case based on the use of carrier particles, is disclosed and described in patent application WO 00/52451. A further example is the competitive assay method as described in patent WO 02/01226. Preferred signal detection methods for screening assays of the instant invention are described in the following patent applications: WO 96/13744, WO 98/16814, WO 98/23942, WO 99/17086, WO 99/34195, WO 00/66985, WO 01/59436, WO 01/59416.

In one further embodiment, the present invention provides a method for producing a medicament comprising the steps of (i) identifying a compound as an inhibitor of binding between a ligand and a gene product of the gene coding for rab31 by the aforementioned inhibitory binding assay and (ii) admixing the compound with a pharmaceutical carrier. However, said compound may also be identifiable by other types of screening assays.

In another aspect, the invention features an assay for testing a compound, preferably for screening a plurality of compounds to determine the degree of binding of said compounds to a translation product of the gene coding for rab31, or to a fragment, or derivative, or variant thereof. Said screening assay comprises (i) adding a liquid suspension of said rab31 translation product, or a fragment, or derivative, or variant thereof, to a plurality of containers, and (ii) adding a detectable, preferably a fluorescently labelled compound or detectable, preferably a plurality of fluorescently labelled compounds to be screened for said binding to said plurality of containers, and (iii) incubating said rab31 translation product, or said fragment, or derivative, or variant thereof, and said detectable, preferably fluorescently labelled compound or said detectable, preferably fluorescently labelled compounds, and (iv) measuring the amounts of preferably fluorescence associated with said rab31 translation product, or with said fragment, or derivative, or variant thereof, and (v) determining the degree of binding by one or more of said compounds to said rab31 translation product, or said fragment, or derivative, or variant thereof. In this type of assay it might be preferred to use a fluorescent label. However, any other type of detectable label might also be employed. Also in this type of assay it might be preferred to reconstitute a rab31 translation product or fragment, or derivative, or variant thereof into artificial liposomes as described in the present invention. Said assay methods may be useful for the identification of novel compounds as well as for evaluating compounds which have been improved or otherwise optimized in their ability to bind to a rab31 translation product, or fragment, or derivative, or variant thereof.

In one further embodiment, the present invention provides a method for producing a medicament comprising the steps of (i) identifying a compound as a binder to a gene product of the rab31 gene by the aforementioned binding assays and (ii) admixing the compound with a pharmaceutical carrier. However, said compound may also be identifiable by other types of screening assays.

In another embodiment, the present invention provides for a medicament obtainable by any of the methods according to the herein claimed screening assays. In one further embodiment, the instant invention provides for a medicament obtained by any of the methods according to the herein claimed screening assays.

The present invention features a protein molecule shown in SEQ ID NO. 1, said protein molecule being a translation product of the gene coding for a rab31 protein, or a fragment, or derivative, or variant thereof, for use as a diagnostic target for detecting a neurodegenerative disease, preferably Alzheimer's disease.

The present invention further features a protein molecule shown in SEQ ID NO. 1, said protein molecule being a translation product of the gene coding for a rab31 protein, or a fragment, or derivative, or variant thereof, for use as a screening target for reagents or compounds preventing, or treating, or ameliorating a neurodegenerative disease, preferably Alzheimer's disease.

The present invention features an antibody which is specifically immunoreactive with an immunogen, wherein said immunogen is a translation product of a gene coding for rab31, SEQ ID NO. 1, or a fragment, or variant, or derivative thereof. The immunogen may comprise immunogenic or antigenic epitopes or portions of a translation product of said gene, wherein said immunogenic or antigenic portion of a translation product is a polypeptide, and wherein said polypeptide elicits an antibody response in an animal, and wherein said polypeptide is immunospecifically bound by said antibody. Methods for generating antibodies are well known in the art (see Harlow et al., *Antibodies, A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1988). The term "antibody", as employed in the present invention, encompasses all forms of antibodies known in the art, such as polyclonal, monoclonal, chimeric, recombinatorial, anti-idiotypic, humanized, or single chain antibodies, as well as fragments thereof (see Dubel and Breitling, *Recombinant Antibodies*, Wiley-Liss, New York, NY, 1999). Antibodies of the present invention are useful, for instance, in a variety of diagnostic and therapeutic methods, based on state-in-the-art techniques (see Harlow and Lane, *Using Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1999 and Edwards R., *Immunodiagnostics: A Practical Approach*, Oxford University Press, Oxford, England, 1999) such as enzyme-immuno assays

(e.g. enzyme-linked immunosorbent assay, ELISA), radioimmuno assays, chemoluminescence-immuno assays, Western-blot, immunoprecipitation and antibody microarrays. These methods involve the detection of translation products of the rab31 gene, or fragments, or derivatives, or variants thereof.

In a preferred embodiment of the present invention, said antibodies can be used for detecting the pathological state of a cell in a sample from a subject, comprising immunocytochemical staining of said cell with said antibody, wherein an altered degree of staining, or an altered staining pattern in said cell compared to a cell representing a known health status indicates a pathological state of said cell. Preferably, the pathological state relates to a neurodegenerative disease, in particular to AD. Immunocytochemical staining of a cell can be carried out by a number of different experimental methods well known in the art. It might be preferred, however, to apply an automated method for the detection of antibody binding, wherein the determination of the degree of staining of a cell, or the determination of the cellular or subcellular staining pattern of a cell, or the topological distribution of an antigen on the cell surface or among organelles and other subcellular structures within the cell, are carried out according to the method described in US patent 6150173.

Other features and advantages of the invention will be apparent from the following description of figures and examples which are illustrative only and not intended to limit the remainder of the disclosure in any way.

Figure 1 depicts the brain regions with selective vulnerability to neuronal loss and degeneration in AD. Primarily, neurons within the inferior temporal lobe, the entorhinal cortex, the hippocampus, and the amygdala are subject to degenerative processes in AD (Terry et al., *Annals of Neurology* 1981, 10:184-192). These brain regions are mostly involved in the processing of learning and memory functions. In contrast, neurons within the frontal cortex, the occipital cortex, and the cerebellum remain largely intact and preserved from neurodegenerative processes in AD. Brain tissues from the frontal cortex (F) and the temporal cortex (T) of AD patients and healthy, age-matched control individuals were used for the herein disclosed examples. For illustrative purposes, the image of a normal healthy brain was taken from a publication by Strange (*Brain Biochemistry and Brain Disorders*, Oxford University Press, Oxford, 1992, p.4).

Figure 2 illustrates the verification of the differential expression of the human rab31 gene in AD brain tissues by quantitative RT-PCR analysis. Quantification of RT-PCR products from RNA samples collected from the frontal cortex (F) and temporal cortex (T) of AD patients (Figure 2a) and of healthy, age-matched control individuals (Figure 2b) was performed by the LightCycler rapid thermal cycling technique. The data were normalized to the combined average values of a set of standard genes which showed no significant differences in their gene expression levels. Said set of standard genes consisted of genes for the ribosomal protein S9, the transferrin receptor, GAPDH, and beta-actin. The figure depicts the kinetics of amplification by plotting the cycle number against the amount of amplified material as measured by its fluorescence. Note that the amplification kinetics of the rab31 cDNA from both the frontal and temporal cortices of a normal control individual during the exponential phase of the reaction are juxtaposed (Figure 2b, arrows), whereas in AD (Figure 2a, arrows), there is a significant separation of the corresponding curves, indicating a differential expression of the rab31 gene in the two analyzed brain regions.

Figure 3 discloses SEQ ID NO. 1, the amino acid sequence of rab31 protein (NCBI GenBank accession number: AAB02832, Q13636). The full length human rab31 protein comprises 194 amino acids.

Figure 4 shows SEQ ID NO. 2, the nucleotide sequence of the human rab31 cDNA coding sequence, comprising 585 nucleotides. The length of rab31 cDNA according to NCBI GenBank entry U59877 is 921 base pairs.

Figure 5 depicts SEQ ID NO. 3, the nucleotide sequence of the 212 bp rab31 cDNA fragment, identified and obtained by suppressive subtractive hybridization (sequence in 5' to 3' direction).

Figure 6 outlines the sequence alignment of SEQ ID NO. 3 to the nucleotide sequence of the human rab31 cDNA (GenBank accession number: AF183421).

Figure 7 depicts human cerebral sections labelled with an affinity-purified rabbit anti-rab31 antiserum (green signals) raised against a peptide corresponding to amino acids 181 to 194 of rab31. Immunoreactivity of rab31 was detected in both

the pre-central cortex (CT) and the white matter (WM) (Figure 7a, low magnification). Strong punctate staining of the cytoplasm appears in the neurons of the cortex (CT) (Figure 7b, high magnification) and in the glial cells of the white matter (WM) (Figure 7c, high magnification) indicating an intracellular membrane-associated localization of rab31. Blue signals indicate nuclei stained with DAPI.

Table 1 discloses the initial identification of differential expression of the human rab31 gene by subtractive suppressive microarray hybridization experiments. Identical biochips containing cDNA clones of subtracted AD and control brain cDNA libraries were co-hybridized with different Cyanine3 (Cy3) and Cyanine5 (Cy5) labeled cDNA probes, designated as probes B or C, respectively. Cy3 and Cy5 labeled SMART probes (B) were generated from cDNAs, derived from frontal or temporal cortex of AD patients and control persons, respectively, refer to section (vi-b). Cy3 and Cy5 labeled SSH probes (C) were derived from cDNA populations after suppressive subtractive hybridization of brain cDNAs from frontal and temporal cortex of AD patients and of control individuals, respectively, refer to section (vi-c); ($PF_{SSH(1)}$ = AD frontal cortex cDNA after subtraction of AD temporal cortex cDNA; $PT_{SSH(2)}$ = AD temporal cortex cDNA after subtraction of AD frontal cortex cDNA). The table lists the gene expression level of rab31 indicated as the ratio of fluorescence intensity measured for the temporal cortex relative to the frontal cortex of AD patients. The ratios of fluorescence intensity reflect a differential regulation of human rab31 RNA expression in temporal and frontal cortex of AD patients.

Table 2 lists rab31 gene expression levels in the temporal cortex relative to the frontal cortex in seven AD patients, herein identified by internal reference numbers P010, P011, P012, P014, P016, P017, P019 (1.04 to 2.43 fold) and five healthy, age-matched control individuals, herein identified by internal reference numbers C005, C008, C011, C012, C014 (0.77 to 1.45 fold). The scatter plot diagram visualizes individual values of the temporal to frontal cortex regulation ratios in control samples (dots) and in AD patient samples (triangles), respectively. The values shown are calculated according to the formula described herein (see below).

EXAMPLE I:

(i) Brain tissue dissection from patients with AD:

Brain tissues from AD patients and age-matched control subjects were collected on average within 5 hours post-mortem and immediately frozen on dry ice. Sample sections from each tissue were fixed in paraformaldehyde for histopathological confirmation of the diagnosis. Brain areas for differential expression analysis were identified (see Figure 1) and stored at -80°C until RNA extractions were performed.

(ii) Isolation of total mRNA:

Total RNA was extracted from post-mortem brain tissue by using the RNeasy kit (Qiagen) according to the manufacturer's protocol. The accurate RNA concentration and the RNA quality were determined with the DNA LabChip system using the Agilent 2100 Bioanalyzer (Agilent Technologies). For additional quality testing of the prepared RNA, i.e. exclusion of partial degradation and testing for DNA contamination, specifically designed intronic GAPDH oligonucleotides and genomic DNA as reference control were used to generate a melting curve with the LightCycler technology as described in the manufacturer's protocol (Roche).

(iii) cDNA synthesis and Rsa I digestion

In order to identify changes in gene expression in different tissues, a screening method combining cDNA synthesis, suppressive subtractive hybridization (SSH) and screening of microarray chips with a diversity of cDNA probes from SSH was employed. This technique compares different populations of mRNA and provides clones of genes that are expressed in one population of cells but not, or at lower level, in the other population of cells. In the present invention, RNA populations from selected post-mortem brain tissues (frontal and temporal cortex) of AD patients and age-matched control subjects were compared.

As starting material for the suppressive subtractive microarray analysis total RNA was extracted as described above (ii). For production of preferably full-length cDNAs, the polymerase chain reaction (PCR)-based method 'SMART cDNA Synthesis' was performed according to the manufacturer's protocol (Clontech).

The principle of 'SMART cDNA synthesis' has been described in detail (Chenchik et al., in *Gene Cloning and Analysis* by RT-PCR, Eds. Siebert and Larrick, *Biotechniques Books*, Natick, MA 1998: 305-320). For SMART cDNA synthesis, four RNA pools, each consisting of 8 µg total RNA, were prepared. Each pool contained 2 µg of each of four different samples, i.e. from inferior frontal cortex (CF) and from inferior temporal cortex (CT) of control brains, from inferior frontal cortex (PF) and from inferior temporal cortex (PT) of patient brains, respectively. An amount of 1 µg

of total RNA mix was utilized in a reaction volume of 50 µl (PCR cycler: Multi Cycler PTC 200, MJ Research). The second SMART PCR step was performed using 19 cycles. SuperScript II RNaseH Reverse Transcriptase and 5x first-strand buffer (Invitrogen) were used.

After extraction and purification of the PCR products, restriction digestions were carried out with 30 U Rsa I (MBI Fermentas) for 2.5 hours at 37°C. Rsa I restriction sites are located within the universal priming sites of the double stranded (ds) cDNA. The quality of the digestions was analyzed by agarose gel electrophoresis, the digested samples were purified (QIAquick PCR Purification Kit, Qiagen), and the cDNA concentrations were determined by UV spectrophotometry (Biorad).

(iv) Suppressive subtractive hybridization (SSH)

Four SMART cDNA pools (iii), were compared using suppressive subtractive hybridization. A pool of cDNA containing differentially expressed genes is thereby designated as "tester", the reference cDNA pool as "driver". The two pools are hybridized, and all cDNAs, present in both pools will be eliminated, i.e. the driver-pool will be subtracted from the tester-pool. Thus, clones of genes that are predominantly expressed in the tester population are obtained.

The 'PCR-Select cDNA Subtraction Kit' (Clontech) was used to perform the subtractive hybridization. The 'tester' SMART cDNA pools, derived from temporal cortex (CT) of control brains, and from frontal and temporal cortex (PF and PT) of patient brains (iii), were subdivided into two pools each. Each pool was ligated with adaptor 1 or adaptor 2, respectively, thus obtaining 6 different 'tester' cDNA pools. The three 'driver' SMART cDNA pools, CT, PF and PT, remained unligated. In a first hybridization step, used to enrich for differentially expressed sequences, the following three different 'tester' SMART cDNA pools were combined with an excess of the following 'driver' SMART cDNAs: SSH(1): PF-'tester' and PT-'driver'; SSH(2): PT-'tester' and PF-'driver'; SSH(3): CT-'tester' and PT-'driver'; SSH(4): PT-'tester' and CT-'driver'. Following a denaturation step for 1.5 min at 98°C, the hybridization was carried out for 8 hours at 68°C. In a second step, the two corresponding primary hybridization samples of 'tester' SMART cDNA pools ligated to adaptor 1 or 2, respectively, were mixed and re-hybridized at 68°C for 15 hours, with an excess of the 'driver' SMART cDNA pool, as used before. Thus, suitable double stranded cDNAs for subsequent amplification, i.e. with both adaptor sequences at their 5' and 3' ends and therefore with different annealing sites, were generated. The following PCR steps were applied to obtain efficiently amplified specific products and to

suppress nonspecific amplification. In the first PCR, missing strands of the adaptors were filled in by DNA-polymerase activity. 1 µl of the obtained hybridization products each were subjected to PCR using the corresponding 'primer 1' (10 µM) (Clontech) along with 1x PCR reaction buffer (Clontech), 10 mM dNTP-Mix (dATP, dGTP, dCTP, dTTP, Amersham Pharmacia Biotech), and 0.5 µl 50x Advantage cDNA Polymerase Mix (Clontech) in a 25 µl final volume. PCR conditions were set as follows: one round at 75 °C for 5 min, which was followed by 27 or 30 cycles: 94 °C for 30 sec, 64 °C or 66 °C for 30 sec, 72 °C for 1.5 min. One final step at 72 °C for 5 min was added to the last cycle. A second nested PCR was performed as described for the first PCR, except that instead of 'primer 1' the nested primers 'nested primer 1' and '2R' were used and an annealing temperature of 66°C or 68°C and 12 or 15 cycles, were applied. PCR-products obtained by different conditions were pooled for subsequent analysis. For the primer sequences used, refer to appendix B of the supplier's user manual (Clontech).

(v) Cloning of subtracted PCR products and production of DNA-biochips

The SSH SMART double stranded cDNAs of the four different combinations SSH(1)-SSH(4), refer to (iv), were ligated into the pCR2.1-vector and transformed into INValphaF' cells according to the manufacturer's instructions (TA Cloning Kit, Invitrogen). Bacterial colonies were picked and analyzed by colony PCR on MTPs (microtiter plates, 96 well, Abgene), using 'nested primer 1' and 'nested primer 2'. Those MTPs showing more than 90% positive clones were subjected to a preparative colony PCR approach. Per well, the following PCR mix was generated: the corresponding oligonucleotides 'nested primer 1' and 'nested primer 2' (0.5 µM each), 1 x Titanium PCR buffer (Clontech), 200 µM dNTP-Mix (Amersham Pharmacia Biotech), 0.2 x TitaniumTaq DNA-Polymerase (Clontech) in a 120 µl final volume. PCR conditions were set as follows: one round at 94 °C for 30 sec for denaturing, the next round was followed by 35 cycles: 94 °C for 30 sec and 68°C for 3 min. The quality of the amplified products was analyzed (DNA LabChip system, Agilent 2100 Bioanalyzer, Agilent Technologies), followed by purification (Multiscreen-PCR-Purification system, Millipore).

Additionally, the following standard control samples were generated: three different *Arabidopsis thaliana* genes, polyA-DNA, salmon sperm DNA, human Cot-1 DNA, and 3xSSC-buffer were used as negative controls (Microarray Validation System, Stratagene); beta-Actin and Xenopus cDNA were used as normalizing controls.

Several MTPs were made of each of the SSH combinations SSH(1)-(4), harboring amplification products of 96 different clones per plate. The amplified products were spotted in triplicates onto GAPS glass-slides (CMT-GAPS, Corning) by GeneScan Europe.

(vi) Probe synthesis and identification of differentially expressed genes by screening of DNA biochips:

B: SMART probe synthesis

For the production of Cyanine3 (Cy3) and Cyanine5 (Cy5) labeled SMART cDNA-probes, the PCR-based method 'SMART cDNA Synthesis' was performed as described in section (iii). Here, total RNA was used as starting material, which had been extracted as described above (ii). Four RNA mixtures were prepared as described in section (iii). 1 µg of each RNA mix and 1 ng Xenopus total RNA were subjected to the SMART cDNA reaction. For PCR amplification, extraction and purification of the cDNAs, restriction digestion with Rsa I, and subsequent purification of the digested samples, refer to section (iii).

SMART cDNA samples were labeled with either Cy3 or Cy5 (Atlas Glass Fluorescent Labeling Kit, Clontech). In the first labeling step, aliphatic amino groups, i.e. aminoallyl-dUTP (Clontech), were incorporated into denatured (100°C, 7 min) Rsa I digested PCR products. The reaction was catalyzed by the Klenow Fragment (MBI Fermentas). In a second labeling step, the fluorescent reporter dyes Cy3 or Cy5 were coupled to the incorporated functionalities. The purified Cy3 and Cy5 labeled SMART cDNA probes (Atlas NucleoSpin Extraction Kit, Clontech) were resuspended in hybridization buffer (5x SSC, 0.1% SDS, 25% formamide) after denaturation for 7 min at 100°C. Subsequently, the Cy3 labeled SMART probe was mixed with the Cy5 labeled SMART probe and together applied evenly onto one prehybridized (5x SSC, 0.1% SDS, 1% BSA, 45 min at 42°C) microarray. Array hybridization was performed over night at 42°C. High stringency washing of the biochips followed according to the instructions of the TSA Detection Kit protocol (NEN Life Science).

Biochip 2 was hybridized with SMART cDNA mix PF(Cy3) and PT(Cy5). Scanning the microarrays with the appropriate wavelengths (635 nm, 532 nm) allowed detection of both cyanine dyes simultaneously.

C: Subtraction probe synthesis

For the production of Cyanine3 (Cy3) and Cyanine5 (Cy5) labeled SSH cDNA-probes, the PCR-based method 'SMART cDNA Synthesis' was performed as

described in section (iii). Here, we used total RNA as starting material, which was extracted as described above (ii). Four RNA mixtures were prepared as disclosed in section (iii). 1 µg of each RNA mix was subjected to the SMART cDNA reaction. For PCR amplification, extraction and purification of the cDNAs, restriction digestion with Rsa I, and subsequent purification of the digested samples, refer to section (iii). For subtractive hybridization, the PCR-Select cDNA Subtraction Kit (Clontech) was utilized as described in detail in section (iv). The subtracted PCR products of the combinations SSH(1) and SSH(2), and of SSH(3) and SSH(4), respectively, were purified (StrataClean Kit, Stratagene), and adaptor 1 and 2 removed by restriction digest with Rsa I and Sma I (MBI Fermentas). The SSH cDNA pools were labeled with either Cy3 or Cy5 (Atlas Glass Fluorescent Labeling Kit, Clontech). In the first labeling step, aliphatic amino groups, i.e. aminoallyl-dUTP (Clontech), were incorporated into the denatured (100°C, 7 min) Rsa I and Sma I digested SSH cDNA products. The reaction was catalyzed by the Klenow Fragment (MBI Fermentas). In a second labeling step, the fluorescent reporter dyes Cy3 and Cy5 were coupled to the incorporated functionalities.

The purified Cy3 and Cy5 labeled SSH cDNA probes (for purification refer to the Atlas NucleoSpin Extraction Kit, Clontech) were resuspended in hybridization buffer (5x SSC, 0.1% SDS, 25% formamide) after denaturation for 7 min at 100°C. Subsequently, the Cy3 labeled SSH1 probe was mixed with the Cy5 labeled SSH2 probe, and the Cy3 labeled SSH3 probe with the Cy5 labeled SSH4 probe, respectively. Each combination was applied evenly onto one prehybridized (5x SSC, 0.1% SDS, 1% BSA, 45 min at 42°C) microarray. Array hybridization was performed over night at 42°C. High stringency washing of the biochips followed according to the instructions of the TSA Detection Kit protocol (NEN Life Science).

Biochip 1 was hybridized with the cDNA mix SSH(1)(Cy3) and SSH(2)(Cy5). Scanning of the microarrays with the appropriate wavelengths (635 nm, 532 nm) allowed detection of both cyanine dyes simultaneously.

(vii) DNA biochips data evaluation

Fluorescence raw data for Cy3 and Cy5, measured at 635 and 532 nm, respectively, were taken severalfold (for each of the three spots per cDNA). One set of measurements was performed within the spot area (signal) and another set of measurements was taken nearby (background). Subsequently the net fluorescence intensity (FI_{635}, FI_{532}) of the spots was calculated as follows:

$$FI_{635/532} = (M\ FI_{spot} - 1\ SD\ FI_{spot}) - (M\ FI_{background} + 1\ SD\ FI_{background}).$$

In this calculation, M defines the median of the replicate measurements per spot, SD the standard deviation of the corresponding mean. Subsequently, only FI_{635} and FI_{532} values of >2 were considered for further evaluation plus those FI_{635} and FI_{532} values of <2 where the corresponding value for the second wavelength was >3.
In an analogous manner, the corresponding values for the Xenopus cDNA control and the set of standard (housekeeping) genes were evaluated. The Xenopus cDNA was used as an internal calibrator for the efficiency of cDNA synthesis of the disease relevant mRNAs. Then, from the background corrected $FI_{635/532}$ medians of the three replicate spots, the statistical mean was calculated and the signal ratio R for the cDNA probes was derived using the formula:

$$R_{635/532} = FI_{635,\ calibrated} / FI_{532,\ calibrated.}$$

In a last step of evaluation, the results of the different hybridizations were considered for logical coherence.

(viii) Confirmation of differential expression by quantitative RT-PCR:
Positive corroboration of differential expression of the gene coding for rab31 was performed using the LightCycler technology (Roche). This technique features rapid thermal cyling for the polymerase chain reaction as well as real-time measurement of fluorescent signals during amplification and therefore allows for highly accurate quantification of RT-PCR products by using a kinetic, rather than an endpoint readout. The ratio of rab31 cDNA from the temporal cortex and frontal cortex was determined (relative quantification).
First, a standard curve was generated to determine the efficiency of the PCR with specific primers for the gene coding for rab31: 5'- ACTGCTGAAGGACCCTACGC-3' and 5'- GATGCAAAGCCAGTGTGCTC-3'. PCR amplification (95 °C and 1 sec, 56 °C and 5 sec, and 72 °C and 5 sec) was performed in a volume of 20 µl containing LightCycler-FastStart DNA Master SYBR Green I mix (contains FastStart Taq DNA polymerase, reaction buffer, dNTP mix with dUTP instead of dTTP, SYBR Green I dye, and 1 mM $MgCl_2$; Roche), 0.5 µM primers, 2 µl of a cDNA dilution series (final concentration of 40, 20, 10, 5, 1 and 0.5 ng human total brain cDNA; Clontech) and, depending on the primers used, additional 5 mM $MgCl_2$. Melting curve analysis revealed a single peak at approximately 85 °C with no visible primer dimers. Quality and size of the PCR product were determined with the DNA LabChip system (Agilent

2100 Bioanalyzer, Agilent Technologies). A single peak at the expected size of 72 bp for the rab31 gene was observed in the electropherogram of the sample.

In an analogous manner, the PCR protocol was applied to determine the PCR efficiency of a set of reference genes which were selected as a reference standard for quantification. In the present invention, the mean value of five such reference genes was determined: (1) cyclophilin B, using the specific primers 5'-ACTGAAGCACTACGGGCCTG-3' and 5'-AGCCGTTGGTGTCTT TGCC-3' except for $MgCl_2$ (an additional 1 mM was added instead of 3 mM). Melting curve analysis revealed a single peak at approximately 87 °C with no visible primer dimers. Agarose gel analysis of the PCR product showed one single band of the expected size (62 bp). (2) Ribosomal protein S9 (RPS9), using the specific primers 5'-GGTCAAATTTACCCTGGCCA-3' and 5'- TCTCATCAAGCGTCAGCAGTTC-3' (exception: additional 1 mM $MgCl_2$ was added instead of 3 mM). Melting curve analysis revealed a single peak at approximately 85°C with no visible primer dimers. Agarose gel analysis of the PCR product showed one single band with the expected size (62 bp). (3) beta-actin, using the specific primers 5'-TGGAACGGTGAAGGTGACA-3' and 5'-GGCAAGGGACTTCCTGTAA-3'. Melting curve analysis revealed a single peak at approximately 87°C with no visible primer dimers. Agarose gel analysis of the PCR product showed one single band with the expected size (142 bp). (4) GAPDH, using the specific primers 5'-CGTCATGGGTGTGAACCATG-3' and 5'-GCTAAGCAGTTGGTGGTGCAG-3'. Melting curve analysis revealed a single peak at approximately 83°C with no visible primer dimers. Agarose gel analysis of the PCR product showed one single band with the expected size (81 bp). (5) Transferrin receptor TRR, using the specific primers 5'-GTCGCTGGTCAGTTCGTGATT-3' and 5'-AGCAGTTGGCTGTTGTACCTCTC-3'. Melting curve analysis revealed a single peak at approximately 83°C with no visible primer dimers. Agarose gel analysis of the PCR product showed one single band with the expected size (80 bp). For calculation of the values, first the logarithm of the cDNA concentration was plotted against the threshold cycle number C_t for rab31 and the five reference standard genes. The slopes and the intercepts of the standard curves (i.e. linear regressions) were calculated for all genes. In a second step, cDNAs from frontal cortex and temporal cortex were analyzed in parallel and normalized to cyclophilin B. The C_t values were measured and converted to ng total brain cDNA using the corresponding standard curves:

$$10 \wedge ((C_t \text{ value} - \text{intercept}) / \text{slope}) \quad [\text{ng total brain cDNA}]$$

The values for frontal and temporal cortex rab31 cDNAs were normalized to cyclophilin B and the ratio was calculated according to formula:

$$\text{Ratio} = \frac{\text{rab31 temporal [ng] / cyclophilin B temporal [ng]}}{\text{rab31 frontal [ng] / cyclophilin B frontal [ng]}}$$

In a third step, the set of reference standard genes was analyzed in parallel to determine the mean average value of the temporal to frontal ratios of expression levels of the reference standard genes for each individual brain sample. As cyclophilin B was analyzed in step 2 and step 3, and the ratio from one gene to another gene remained constant in different runs, it was possible to normalize the values for rab31 to the mean average value of the set of reference standard genes instead of normalizing to one single gene alone. The calculation was performed by dividing the ratio shown above by the deviation of cyclophilin B from the mean value of all housekeeping genes. The results of one such quantitative RT-PCR analysis for the rab31 gene are shown in Figure 2.

(ix) Immunohistochemistry:

For immunofluorescence staining of rab31 in human brain, frozen sections were prepared with a cryostat (Leica CM3050S) from post-mortem pre-central gyrus of a donor person and fixed in 4% PFA for 20 min. After washing in PBS, the sections were pre-incubated with blocking buffer (10% normal goat serum, 0.2% Triton X-100 in PBS) for 30 min, and then incubated with affinity-purified rabbit anti-rab31 antisera (1:30-40 diluted in blocking buffer; custom-made, Davids Biotechnologie, Regensburg) overnight at 4°C. After rinsing three times in 0.1% Triton X-100/PBS, the sections were incubated with FITC-conjugated goat anti-rabbit IgG (1:150 diluted in 1% BSA/PBS) for 2 hours at room temperature and then again washed in PBS. Staining of the nuclei was performed by incubation of the sections with 5µM DAPI in PBS for 3 min (blue signal). In order to block the autofluoresence of lipofuscin in human brain, the sections were treated with 1% Sudan Black B in 70% ethanol for 2-10 min at room temperature and then sequentially dipped in 70% ethanol, destilled water and PBS. The sections were coverslipped with 'Vectrashield' mounting medium (Vector Laboratories, Burlingame, CA) and observed under an inverted

microscope (IX81, Olympus Optical). The digital images were captured with the appropriate software (AnalySiS, Olympus Optical).

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